



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 8, 2026 – 03:09 AM UTC

PDB ID : 4QGB / pdb_00004qgb
Title : Crystal structure of mutant ribosomal protein G219V TthL1
Authors : Gabdulkhakov, A.G.; Nevskaya, N.A.; Nikonov, S.V.
Deposited on : 2014-05-22
Resolution : 2.60 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity	:	4-5-2 with Phenix2.0
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

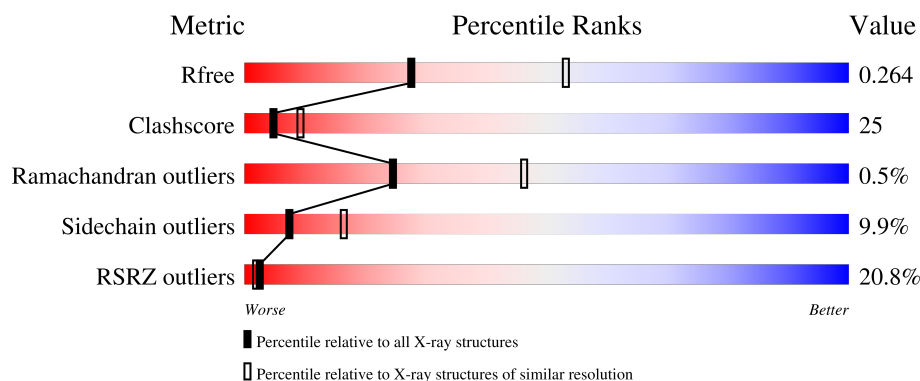
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.60 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	180053	4008 (2.60-2.60)
Clashscore	190562	4347 (2.60-2.60)
Ramachandran outliers	187476	4277 (2.60-2.60)
Sidechain outliers	187428	4277 (2.60-2.60)
RSRZ outliers	180081	4008 (2.60-2.60)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	216	
1	B	216	

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
3	ACT	A	302	-	-	X	-

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 3331 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the ZeroOcc column contains the number of atoms modelled with zero occupancy, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called 50S ribosomal protein L1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	216	Total	C	N	O	S	0	0	0
			1642	1039	296	304	3			
1	B	216	Total	C	N	O	S	0	0	0
			1642	1039	296	304	3			

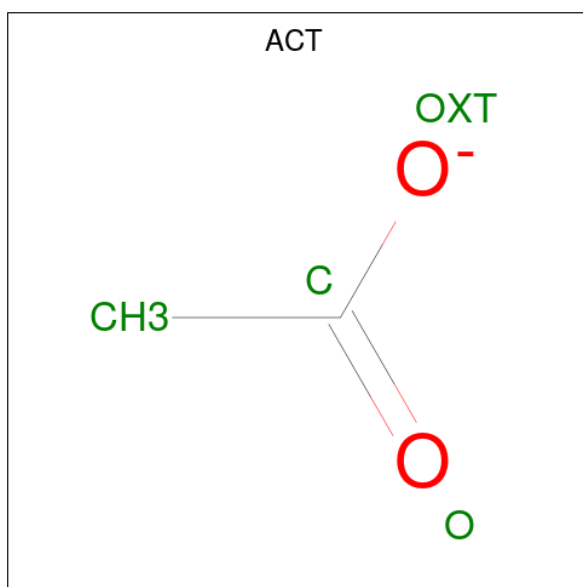
There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	219	VAL	GLY	engineered mutation	UNP P27150
B	219	VAL	GLY	engineered mutation	UNP P27150

- Molecule 2 is CHLORIDE ION (CCD ID: CL) (formula: Cl).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	1	Total	Cl	0	0
			1	1		
2	B	2	Total	Cl	0	0
			2	2		

- Molecule 3 is ACETATE ION (CCD ID: ACT) (formula: C₂H₃O₂).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	C	O	0	0
			4	2	2		

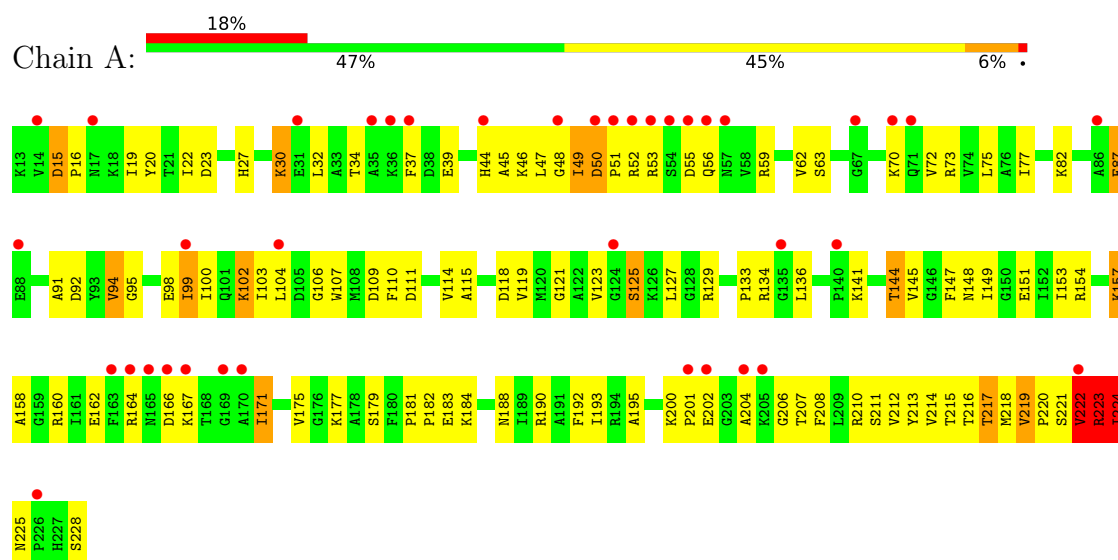
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	22	Total	O	0	0
			22	22		
4	B	18	Total	O	0	0
			18	18		

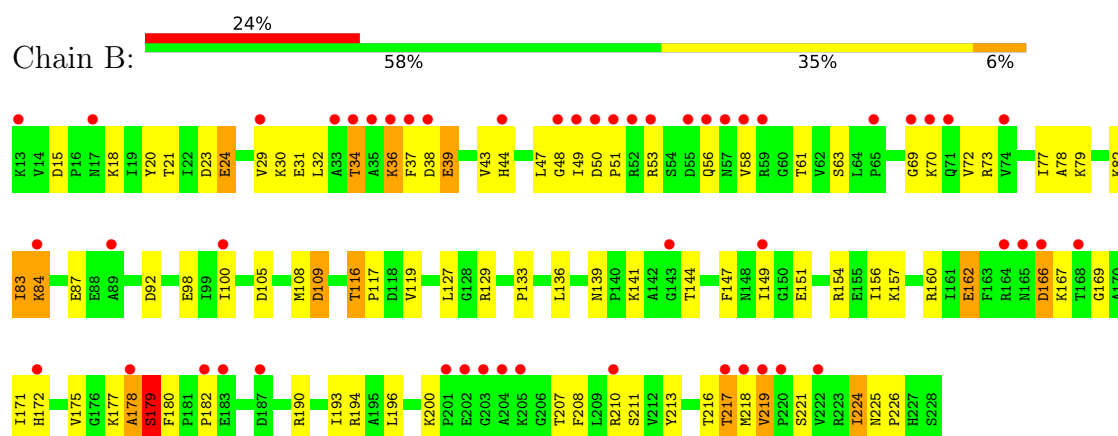
3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density ($RSRZ > 2$). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

• Molecule 1: 50S ribosomal protein L1



• Molecule 1: 50S ribosomal protein L1



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	66.53Å 74.75Å 87.06Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	36.43 – 2.60 36.43 – 2.60	Depositor EDS
% Data completeness (in resolution range)	93.0 (36.43-2.60) 93.2 (36.43-2.60)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.05 (at 2.61Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.8.4_1496)	Depositor
R, R_{free}	0.226 , 0.251 0.249 , 0.264	Depositor DCC
R_{free} test set	663 reflections (4.77%)	wwPDB-VP
Wilson B-factor (Å ²)	28.2	Xtriage
Anisotropy	1.277	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.39 , 72.7	EDS
L-test for twinning ²	$\langle L \rangle = 0.45$, $\langle L^2 \rangle = 0.29$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.85	EDS
Total number of atoms	3331	wwPDB-VP
Average B, all atoms (Å ²)	33.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 20.16 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 9.2355e-03. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: ACT, CL

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	A	0.76	1/1672 (0.1%)	1.17	11/2258 (0.5%)
1	B	0.74	0/1672	1.13	10/2258 (0.4%)
All	All	0.75	1/3344 (0.0%)	1.15	21/4516 (0.5%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	1
1	B	0	2
All	All	0	3

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	72	VAL	C-O	-5.32	1.18	1.23

All (21) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	15	ASP	CA-C-N	7.15	126.40	118.97
1	A	15	ASP	C-N-CA	7.15	126.40	118.97
1	B	109	ASP	N-CA-C	6.84	121.23	113.02
1	A	222	VAL	N-CA-C	-6.70	98.53	108.99
1	B	224	ILE	N-CA-C	6.58	116.56	108.53
1	B	108	MET	N-CA-C	6.14	120.91	113.17
1	B	78	ALA	N-CA-C	6.08	116.59	108.38
1	B	219	VAL	CA-C-N	-5.65	112.78	119.84

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	219	VAL	C-N-CA	-5.65	112.78	119.84
1	B	225	ASN	CA-C-N	5.62	125.72	119.32
1	B	225	ASN	C-N-CA	5.62	125.72	119.32
1	A	219	VAL	CA-C-N	5.57	125.67	119.32
1	A	219	VAL	C-N-CA	5.57	125.67	119.32
1	A	50	ASP	CA-C-N	5.52	125.87	119.47
1	A	50	ASP	C-N-CA	5.52	125.87	119.47
1	A	224	ILE	N-CA-C	5.43	117.62	109.20
1	A	223	ARG	N-CA-C	-5.30	100.53	109.07
1	A	99	ILE	N-CA-C	5.16	115.38	110.42
1	A	222	VAL	N-CA-CB	-5.08	103.94	112.47
1	B	116	THR	CA-C-N	5.02	124.46	119.24
1	B	116	THR	C-N-CA	5.02	124.46	119.24

There are no chirality outliers.

All (3) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	206	GLY	Peptide
1	B	179	SER	Peptide
1	B	217	THR	Peptide

5.2 Too-close contacts

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	1642	0	1688	102	0
1	B	1642	0	1688	84	0
2	A	1	0	0	1	0
2	B	2	0	0	1	0
3	A	4	0	3	2	0
4	A	22	0	0	1	0
4	B	18	0	0	5	0
All	All	3331	0	3379	170	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 25.

All (170) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:38:ASP:OD1	1:B:178:ALA:HB3	1.55	1.05
1:A:27:HIS:HB3	4:A:415:HOH:O	1.79	0.82
1:B:32:LEU:HD23	1:B:219:VAL:HG11	1.60	0.82
1:A:212:VAL:HG23	1:A:224:ILE:HG13	1.61	0.81
1:B:162:GLU:HB3	4:B:411:HOH:O	1.83	0.79
1:A:200:LYS:HE2	3:A:302:ACT:H1	1.64	0.78
1:A:133:PRO:HD3	1:B:133:PRO:HB3	1.65	0.77
1:B:73:ARG:NH1	1:B:109:ASP:O	2.24	0.71
1:A:77:ILE:HG22	1:A:119:VAL:HG21	1.72	0.71
1:A:184:LYS:O	1:A:188:ASN:ND2	2.25	0.69
1:B:15:ASP:HB3	1:B:18:LYS:HB3	1.73	0.69
1:A:47:LEU:HD11	1:A:171:ILE:HD12	1.76	0.68
1:A:141:LYS:HA	1:A:164:ARG:HB3	1.76	0.67
1:A:34:THR:HG21	1:B:218:MET:HE1	1.78	0.65
1:A:44:HIS:CE1	1:B:129:ARG:HE	2.14	0.65
1:A:149:ILE:O	1:A:153:ILE:HG13	1.96	0.65
1:A:216:THR:OG1	1:A:219:VAL:HG22	1.97	0.65
1:A:56:GLN:HB3	1:A:201:PRO:HG3	1.79	0.65
1:A:50:ASP:H	1:A:56:GLN:HG3	1.61	0.65
1:A:129:ARG:HG2	1:B:44:HIS:NE2	2.12	0.65
1:B:218:MET:O	1:B:219:VAL:HG13	1.98	0.63
1:A:102:LYS:O	1:A:107:TRP:HB3	1.99	0.63
1:A:183:GLU:HG2	1:A:184:LYS:HD3	1.80	0.62
1:A:129:ARG:NH1	1:B:133:PRO:O	2.32	0.62
1:A:166:ASP:OD1	1:A:167:LYS:N	2.31	0.61
1:A:91:ALA:HB2	1:A:153:ILE:HD13	1.83	0.61
1:A:121:GLY:O	1:A:125:SER:HB3	2.00	0.60
1:A:27:HIS:CD2	1:A:30:LYS:HZ3	2.19	0.60
1:B:48:GLY:HA2	1:B:210:ARG:HD2	1.84	0.59
1:A:110:PHE:HE1	1:A:136:LEU:HD13	1.68	0.59
1:B:207:THR:HG23	2:B:301:CL:CL	2.40	0.58
1:A:92:ASP:OD1	1:A:157:LYS:NZ	2.36	0.58
1:A:223:ARG:HG3	1:B:105:ASP:OD1	2.04	0.58
1:B:141:LYS:HE3	1:B:167:LYS:HZ2	1.70	0.57
1:B:216:THR:OG1	1:B:219:VAL:HG22	2.05	0.57
1:B:39:GLU:HB3	1:B:217:THR:OG1	2.04	0.57
1:B:207:THR:HG22	1:B:208:PHE:N	2.20	0.57
1:A:37:PHE:CZ	1:B:218:MET:HE3	2.40	0.56
1:A:114:VAL:HG12	1:A:144:THR:HG22	1.87	0.56
1:B:47:LEU:HD23	1:B:58:VAL:HG21	1.88	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:115:ALA:O	1:A:145:VAL:HA	2.06	0.56
1:B:50:ASP:N	1:B:56:GLN:OE1	2.34	0.55
1:A:123:VAL:HG22	1:A:127:LEU:HD12	1.89	0.55
1:A:200:LYS:HD3	1:A:208:PHE:CD1	2.43	0.54
1:A:87:GLU:HB3	1:A:94:VAL:HG21	1.89	0.54
1:B:39:GLU:HB3	1:B:217:THR:HG1	1.72	0.54
1:A:62:VAL:HG11	1:A:192:PHE:HA	1.89	0.54
1:A:141:LYS:NZ	1:A:167:LYS:HE3	2.23	0.54
1:A:214:VAL:H	1:A:222:VAL:HG12	1.73	0.54
1:A:225:ASN:ND2	1:A:228:SER:HB3	2.23	0.54
1:A:148:ASN:ND2	1:A:151:GLU:OE1	2.30	0.54
1:A:207:THR:HG23	3:A:302:ACT:O	2.07	0.54
1:B:98:GLU:H	1:B:98:GLU:CD	2.16	0.54
1:A:82:LYS:HE3	1:A:147:PHE:HB3	1.89	0.53
1:A:16:PRO:HA	1:B:105:ASP:O	2.08	0.53
1:A:215:THR:HG22	1:A:220:PRO:O	2.08	0.53
1:A:213:TYR:CE2	1:A:223:ARG:HG2	2.44	0.53
1:B:49:ILE:HB	1:B:56:GLN:HG2	1.90	0.53
1:A:153:ILE:O	1:A:157:LYS:HB2	2.09	0.52
1:B:117:PRO:HG2	1:B:147:PHE:CZ	2.44	0.52
1:B:177:LYS:O	1:B:179:SER:N	2.43	0.52
1:B:194:ARG:NH2	4:B:403:HOH:O	2.24	0.52
1:A:214:VAL:HG23	1:A:224:ILE:HD13	1.90	0.52
1:B:116:THR:HG23	1:B:149:ILE:HD12	1.91	0.52
1:A:100:ILE:HG13	1:A:127:LEU:HD11	1.91	0.51
1:A:56:GLN:N	1:A:56:GLN:OE1	2.43	0.51
1:A:103:ILE:O	1:A:106:GLY:N	2.28	0.51
1:A:213:TYR:CD2	1:A:223:ARG:HG2	2.45	0.51
1:B:38:ASP:HB3	1:B:177:LYS:NZ	2.25	0.51
1:A:27:HIS:CD2	1:A:30:LYS:NZ	2.78	0.51
1:A:154:ARG:O	1:A:158:ALA:N	2.38	0.51
1:B:38:ASP:O	1:B:177:LYS:NZ	2.44	0.51
1:A:214:VAL:HB	1:A:222:VAL:CG1	2.41	0.51
1:B:211:SER:HB3	1:B:213:TYR:CZ	2.46	0.51
1:A:63:SER:OG	1:A:160:ARG:HG2	2.10	0.50
1:B:69:GLY:HA2	1:B:180:PHE:HZ	1.75	0.50
1:B:139:ASN:H	1:B:144:THR:HG1	1.61	0.49
1:A:134:ARG:HA	1:A:217:THR:HG22	1.94	0.49
1:A:181:PRO:HB2	1:A:184:LYS:HG2	1.94	0.49
1:A:48:GLY:O	1:A:49:ILE:HG23	2.12	0.49
1:A:50:ASP:OD2	1:A:52:ARG:HB2	2.13	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:183:GLU:H	1:A:183:GLU:CD	2.20	0.49
1:B:100:ILE:HG23	1:B:127:LEU:HG	1.94	0.49
1:A:111:ASP:HB3	1:A:177:LYS:HE3	1.95	0.48
1:B:51:PRO:HG3	1:B:169:GLY:HA2	1.94	0.48
1:B:69:GLY:HA2	1:B:180:PHE:CZ	2.48	0.48
1:A:34:THR:HG22	2:A:301:CL:CL	2.50	0.48
1:A:30:LYS:HE2	1:A:30:LYS:HB2	1.55	0.48
1:A:52:ARG:HH11	1:A:52:ARG:HG3	1.79	0.48
1:A:98:GLU:OE1	1:A:98:GLU:N	2.34	0.48
1:A:32:LEU:HD22	1:B:36:LYS:HG2	1.96	0.48
1:B:141:LYS:HE3	1:B:167:LYS:NZ	2.28	0.48
1:A:82:LYS:NZ	1:A:147:PHE:O	2.43	0.48
1:A:75:LEU:HG	1:A:77:ILE:CD1	2.44	0.47
1:B:200:LYS:HE3	1:B:208:PHE:HB2	1.96	0.47
1:A:23:ASP:OD1	1:A:190:ARG:NH2	2.47	0.47
1:A:214:VAL:HB	1:A:222:VAL:HG12	1.97	0.47
1:A:214:VAL:HG23	1:A:224:ILE:CD1	2.44	0.47
1:B:30:LYS:HD3	1:B:182:PRO:HD3	1.96	0.47
1:B:51:PRO:HG3	1:B:169:GLY:CA	2.44	0.47
1:B:171:ILE:HD13	1:B:196:LEU:HD21	1.97	0.47
1:A:53:ARG:NH1	1:A:55:ASP:HB2	2.30	0.47
1:B:207:THR:HG22	1:B:208:PHE:H	1.79	0.47
1:B:31:GLU:HG3	1:B:32:LEU:HD13	1.95	0.47
1:B:79:LYS:HG3	1:B:119:VAL:HG23	1.97	0.47
1:A:46:LYS:N	1:A:211:SER:O	2.41	0.46
1:B:29:VAL:HG13	1:B:216:THR:HG21	1.97	0.46
1:A:44:HIS:HA	1:A:171:ILE:O	2.16	0.46
1:B:21:THR:OG1	1:B:24:GLU:HB2	2.16	0.46
1:A:19:ILE:HD12	1:A:223:ARG:HE	1.80	0.46
1:B:166:ASP:N	1:B:166:ASP:OD1	2.48	0.46
1:A:19:ILE:HD11	1:A:223:ARG:HH21	1.81	0.45
1:A:45:ALA:HA	1:A:211:SER:O	2.17	0.45
1:A:133:PRO:HD3	1:B:133:PRO:CB	2.43	0.45
1:B:47:LEU:C	1:B:49:ILE:H	2.23	0.45
1:B:193:ILE:HD13	1:B:226:PRO:HA	1.98	0.45
1:A:73:ARG:NH1	1:A:109:ASP:OD2	2.48	0.45
1:B:37:PHE:CD1	1:B:37:PHE:O	2.70	0.45
1:A:73:ARG:HH12	1:A:109:ASP:CG	2.23	0.45
1:B:77:ILE:HG22	1:B:119:VAL:HG11	1.99	0.45
1:B:48:GLY:N	1:B:208:PHE:O	2.47	0.45
1:A:44:HIS:ND1	1:B:129:ARG:NE	2.65	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:30:LYS:HE2	1:B:30:LYS:HB3	1.74	0.44
1:B:84:LYS:O	1:B:87:GLU:N	2.46	0.44
1:B:147:PHE:C	1:B:149:ILE:H	2.25	0.44
1:A:104:LEU:HA	1:B:221:SER:HB2	2.00	0.43
1:A:20:TYR:O	1:A:224:ILE:HG22	2.18	0.43
1:A:52:ARG:HG3	1:A:52:ARG:NH1	2.33	0.43
1:B:34:THR:OG1	1:B:218:MET:SD	2.70	0.43
1:B:82:LYS:HE2	1:B:147:PHE:O	2.18	0.43
1:A:27:HIS:HA	1:A:30:LYS:HD3	2.01	0.43
1:B:154:ARG:HD3	1:B:154:ARG:HA	1.65	0.43
1:B:211:SER:HB3	1:B:213:TYR:OH	2.18	0.43
1:A:94:VAL:HG12	1:A:95:GLY:H	1.82	0.43
1:A:193:ILE:HD13	1:A:193:ILE:HA	1.78	0.43
1:A:107:TRP:NE1	1:A:109:ASP:HB3	2.34	0.43
1:B:83:ILE:HD13	1:B:83:ILE:HG21	1.79	0.43
1:A:75:LEU:HD11	1:A:99:ILE:HG21	2.01	0.43
1:B:63:SER:HA	1:B:160:ARG:HB2	2.01	0.42
1:B:177:LYS:C	1:B:179:SER:N	2.77	0.42
1:A:39:GLU:HB3	1:A:217:THR:HG23	2.01	0.42
1:A:201:PRO:HG2	1:A:204:ALA:HB2	2.00	0.42
1:A:218:MET:HE1	1:B:218:MET:SD	2.59	0.42
1:B:151:GLU:O	1:B:154:ARG:N	2.52	0.42
1:A:15:ASP:HA	1:A:16:PRO:HD2	1.73	0.42
1:A:134:ARG:NH2	1:B:219:VAL:HA	2.34	0.42
1:B:43:VAL:HG23	1:B:175:VAL:HG21	2.01	0.42
1:B:72:VAL:HG11	1:B:156:ILE:HG22	2.02	0.42
1:B:73:ARG:HA	1:B:92:ASP:CG	2.45	0.42
1:B:36:LYS:N	1:B:36:LYS:HD2	2.35	0.42
1:B:217:THR:HG21	4:B:406:HOH:O	2.19	0.41
1:A:219:VAL:HG23	1:A:219:VAL:O	2.20	0.41
1:B:117:PRO:HG2	1:B:147:PHE:CE1	2.54	0.41
1:A:59:ARG:CZ	1:A:164:ARG:HD2	2.50	0.41
1:B:20:TYR:HB2	1:B:224:ILE:HG22	2.02	0.41
1:A:100:ILE:HD12	1:A:100:ILE:H	1.85	0.41
1:B:38:ASP:HB3	1:B:177:LYS:HE3	2.02	0.41
1:A:44:HIS:CE1	1:B:129:ARG:NE	2.85	0.41
1:A:46:LYS:HB2	1:A:210:ARG:HB3	2.01	0.41
1:A:48:GLY:N	1:A:208:PHE:O	2.47	0.41
1:A:50:ASP:HA	1:A:51:PRO:HD2	1.82	0.41
1:A:62:VAL:HB	1:A:195:ALA:CB	2.51	0.41
1:B:61:THR:HB	4:B:410:HOH:O	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:38:ASP:HB3	1:B:177:LYS:CE	2.51	0.41
1:A:37:PHE:CE2	1:B:218:MET:HE3	2.56	0.40
1:A:200:LYS:HG3	1:A:201:PRO:HD2	2.03	0.40
1:B:23:ASP:CG	1:B:190:ARG:HH22	2.30	0.40
1:A:30:LYS:HD3	1:A:182:PRO:HB3	2.02	0.40
1:A:141:LYS:HZ3	1:A:167:LYS:HE3	1.86	0.40
1:B:200:LYS:HD3	4:B:416:HOH:O	2.21	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	214/216 (99%)	199 (93%)	14 (6%)	1 (0%)	24	46
1	B	214/216 (99%)	205 (96%)	8 (4%)	1 (0%)	24	46
All	All	428/432 (99%)	404 (94%)	22 (5%)	2 (0%)	24	46

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	49	ILE
1	B	178	ALA

5.3.2 Protein sidechains [i](#)

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	171/171 (100%)	151 (88%)	20 (12%)	5	11
1	B	171/171 (100%)	157 (92%)	14 (8%)	10	24
All	All	342/342 (100%)	308 (90%)	34 (10%)	7	16

All (34) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	22	ILE
1	A	30	LYS
1	A	70	LYS
1	A	87	GLU
1	A	94	VAL
1	A	102	LYS
1	A	118	ASP
1	A	125	SER
1	A	144	THR
1	A	157	LYS
1	A	162	GLU
1	A	171	ILE
1	A	175	VAL
1	A	179	SER
1	A	202	GLU
1	A	217	THR
1	A	221	SER
1	A	222	VAL
1	A	223	ARG
1	A	224	ILE
1	B	24	GLU
1	B	34	THR
1	B	36	LYS
1	B	39	GLU
1	B	53	ARG
1	B	70	LYS
1	B	83	ILE
1	B	84	LYS
1	B	136	LEU
1	B	157	LYS
1	B	162	GLU
1	B	166	ASP
1	B	172	HIS
1	B	179	SER

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (3) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	27	HIS
1	A	101	GLN
1	B	101	GLN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 4 ligands modelled in this entry, 3 are monoatomic - leaving 1 for Mogul analysis.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
3	ACT	A	302	-	3,3,3	0.79	0	3,3,3	1.53	0

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	302	ACT	2	0

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data

6.1 Protein, DNA and RNA chains

In the following table, the column labelled ‘#RSRZ > 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q < 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	216/216 (100%)	1.34	39 (18%) 3 3	13, 28, 57, 88	0
1	B	216/216 (100%)	1.33	51 (23%) 2 1	12, 30, 59, 89	0
All	All	432/432 (100%)	1.34	90 (20%) 2 2	12, 29, 59, 89	0

All (90) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	56	GLN	5.9
1	B	69	GLY	4.6
1	A	55	ASP	4.2
1	A	53	ARG	4.2
1	A	204	ALA	4.1
1	B	50	ASP	4.0
1	B	217	THR	3.8
1	A	57	ASN	3.8
1	A	50	ASP	3.7
1	B	52	ARG	3.7
1	B	34	THR	3.5
1	B	219	VAL	3.5
1	A	201	PRO	3.4
1	B	33	ALA	3.4
1	B	35	ALA	3.4
1	A	205	LYS	3.3
1	B	204	ALA	3.3
1	A	54	SER	3.3
1	B	201	PRO	3.1
1	A	165	ASN	3.1
1	B	168	THR	3.1
1	A	35	ALA	3.1
1	A	202	GLU	3.1
1	B	38	ASP	3.1

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Mol	Chain	Res	Type	RSRZ
1	B	172	HIS	3.0
1	B	36	LYS	3.0
1	A	51	PRO	3.0
1	B	51	PRO	3.0
1	A	166	ASP	2.9
1	B	89	ALA	2.8
1	A	17	ASN	2.8
1	B	57	ASN	2.8
1	A	222	VAL	2.8
1	A	52	ARG	2.7
1	A	169	GLY	2.7
1	A	37	PHE	2.7
1	B	187	ASP	2.7
1	A	71	GLN	2.6
1	A	170	ALA	2.6
1	B	202	GLU	2.6
1	B	203	GLY	2.6
1	A	70	LYS	2.5
1	A	86	ALA	2.5
1	B	74	VAL	2.5
1	B	70	LYS	2.5
1	B	37	PHE	2.5
1	A	36	LYS	2.5
1	A	167	LYS	2.5
1	B	166	ASP	2.5
1	B	13	LYS	2.4
1	A	124	GLY	2.4
1	B	55	ASP	2.4
1	B	65	PRO	2.4
1	A	44	HIS	2.4
1	A	14	VAL	2.3
1	B	178	ALA	2.3
1	B	56	GLN	2.3
1	B	222	VAL	2.3
1	B	183	GLU	2.3
1	B	205	LYS	2.3
1	A	140	PRO	2.3
1	B	164	ARG	2.3
1	B	220	PRO	2.3
1	A	135	GLY	2.3
1	A	164	ARG	2.3
1	B	49	ILE	2.2

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Mol	Chain	Res	Type	RSRZ
1	B	218	MET	2.2
1	B	53	ARG	2.2
1	B	71	GLN	2.2
1	A	67	GLY	2.2
1	A	104	LEU	2.2
1	B	58	VAL	2.2
1	A	48	GLY	2.2
1	B	84	LYS	2.2
1	B	210	ARG	2.2
1	A	99	ILE	2.2
1	A	226	PRO	2.1
1	B	182	PRO	2.1
1	B	143	GLY	2.1
1	B	48	GLY	2.1
1	B	29	VAL	2.1
1	A	163	PHE	2.1
1	A	88	GLU	2.1
1	B	59	ARG	2.1
1	B	165	ASN	2.1
1	B	100	ILE	2.1
1	A	31	GLU	2.0
1	B	149	ILE	2.0
1	B	44	HIS	2.0
1	B	17	ASN	2.0

6.2 Non-standard residues in protein, DNA, RNA chains [i](#)

There are no non-standard protein/DNA/RNA residues in this entry.

6.3 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

6.4 Ligands [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
3	ACT	A	302	4/4	0.62	0.18	27,33,40,41	0
2	CL	B	302	1/1	0.67	0.16	62,62,62,62	0
2	CL	A	301	1/1	0.90	0.15	38,38,38,38	0
2	CL	B	301	1/1	0.93	0.14	22,22,22,22	0

6.5 Other polymers [i](#)

There are no such residues in this entry.